AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows:

Please replace the third paragraph on page 12 with the following:

Fig. 2 shows the mass spectroscopic analysis of (A) non-modified and (B) $^{1}H_3/^{2}D_3$-acylated peptides. (C) Mass spectroscopic analysis of a peptide mixture that, as an example, contains the non-modified peptide as well as the $^{1}H_3$-acylated peptide, and the $^{2}D_3$-acylated peptide with the amino acid sequence EVNGLISMY (SEQ ID NO: 37); (D) explains the nomenclature used in Fig. 2;

Please replace the fourth paragraph on page 12 with the following:

Fig. 3 shows a comparative quantification of antigenic peptides from two different sources, wherein in (A) a mass spectroscopic analysis of the relative amount ratios of three different peptides from two tissue samples (colon cancer sample, sample of healthy tissue from the same patient) is shown. The peptides isolated from the colon cancer sample were $^{2}D_3$-acylated peptide. The peptides isolated from the sample of healthy tissue were $^{1}H_3$-acylated. (B) shows a mass spectroscopic analysis of $^{1}H_4$-nicotinated/guadinated Awells cells, and Awells cells transfected with keratin 18, and $^{2}D_4$-nicotinated/guadinated Awells cells. (C) shows the determination of the amino acid sequences of an $^{1}H_3$-acylated peptide with the amino acid sequence DAAHPTNVQR (SEQ ID NO: 12) and of an $^{1}D_3$-acylated peptide with the amino acid sequence DAAHPTNVQR (SEQ ID NO: 12) by fragmentation;

Please replace the fifth paragraph on page 12 with the following:

Fig. 4 shows yields of peptides that have been chemically modified in four different ways. Four peptides with the amino acid sequences AETSYVKVL (SEQ ID NO: 38), KLSLGLPGL

(SEQ ID NO: 39), SLGLQLAKV (SEQ ID NO: 40) and VLDPRGIYL (SEQ ID NO: 41) were used in a mixture in equimolar amounts, and were subsequently for the purpose of the comparative examination of the three strategies for chemical modification either acylated, or acylated and guadinated, or guadinated and nicotinated. After finalization of the chemical reaction for modification of the reference peptides, these were mixed with the initially used non-modified peptides in order to allow for a comparison in the following analytic step. The comparative evaluation was performed by analysis with nano-electrospray-ionisation-mass spectrometry (nano-ESI-MS).

Please replace the first full paragraph on page 16 with the following:

The online fragmentation of peptides for determining the amino acid sequence (HPLC-MSMS) was performed with an integration time for the "time of flight"-analysis (TOF analyzer) of 4 seconds and a retention time between two analyses of 1/10 seconds and, apart from this, was performed as described. During the process, the online-fragmentation of the $[M+H]^+$ and $[M+H]^{2+}$-ions was automatically switched between the HPLC-MS- and the HPLC-MSMS-modus. The spectra resulting from the mass spectrometric analyses were analysed manually. NCBInr and EST were used as databases with the use of MASCOT ~~(http://www.matrixscience.com)~~ software available from Matrix Science Ltd. (London, U.K.).